

Wed Jul 13 13:49:43 2005

us-09-788-074-4.rnpn

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 17:41:25 ; Search time 1316.5 Seconds
(without alignments)
2368.781 Million cell updates/sec

Title: US-09-788-074-4

Perfect score: 662
Sequence: 1 accgcgcgacgcagaccctc.....taataaatgtttgtgtct 662

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16258531 seqs, 2355356875 residues

Total number of hits satisfying chosen parameters: 32517062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/prodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/prodata/2/pna/PCT_NEW_COMB.seq2:*
3: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq2:*
9: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq3:*
10: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq4:*
11: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq5:*
12: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq6:*
13: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq:*
14: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq2:*
15: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq3:*
16: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq4:*
17: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Wed Jul 13 13:49:43 2005

US-09-788-074-4.rupm

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:01:50 ; Search time 3043.97 Seconds
(without alignments)
8878.154 Million cell updates/sec

Title: US-09-788-074-4

Perfect score: 662

Sequence: 1 accgcgcgcgcgcaccctc.....taataaatgtgttgct 662

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext: 1.0

Searched: 4554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :